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<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US4.DIV

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<141> 2001-11-13

<150> US 09/924,340

<151> 2001-08-06

<150> PCT/IB01/01715

<151> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 112

<170> JPatent

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cggttgccaca gttttgatga tcatctctct cccaaccaag atggtggaaa aagcaaaaac 180

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Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr
      35      40      45
Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr
      50      55      60
Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu
      65      70      75      80
Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu
      85      90      95
Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu
      100      105      110
Ile Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met
      115      120      125
Lys Gln Lys Gly Lys Lys
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                                     -25      -20
cgc tct ccc gtc ccg cgg tgg ttg ctg ctg ccg ctg ctg ctg ggc 104
Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Pro Leu Leu Leu Gly
      -15      -10      -5
ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa 152
Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
      1      5      10
gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg 200
Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp
      15      20      25
ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg 248
Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu
      30      35      40      45
gtc atg tgg ctt cag ggc ggt cca ggc ggt tct agc act gga ttt gga 296
Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly
      50      55      60
aac ttt gag gaa att ggg ccc ctt gac agt gat ctc aaa cca cgg aaa 344
Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys
      65      70      75

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acc acc tgg ctc cag gct gcc agt ctc cta ttt gtg gat aat ccc gtg 392
Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val
80 85 90
ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac 440
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp
95 100 105
ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc 488
Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
110 115 120 125
agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag 536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu
130 135 140
tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag 584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys
145 150 155
gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg 632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu
160 165 170
ggg gat tcc tgg atc tcc cct gtt gat tgc gtg ctc tcc tgg gga cct 680
Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro
175 180 185
tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg 728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val
190 195 200 205
tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac 776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr
210 215 220
aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag 824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln
225 230 235
gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt 872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly
240 245 250
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac 917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His
255 260 265
tgaggctccc cacatatctg caaatgattg catgctggat aataaatctc ttgggtctaa 977
gcagtgatgt agtggctcct tacagagtca gaaagccacc caggcctgca agacttgctt 1037
gtccttcact aaatgtatgg attctattaa aaaaaaaaaa aaaa 1081

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Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
-10 -5 1 5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
10 15 20
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
25 30 35
Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
40 45 50
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
55 60 65 70
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu

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Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
25          30          35          40
aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
          45          50          55
tca att gtc act tgatgatata attgcaattt aaactggttaa gctgtgttca 357
Ser Ile Val Thr
          60
gtactgtttc tgaataatag aaatcacttc tctaaaagca ataaatttca agcacatttt 417
taaataaaaa aaaaaaaaaa a 438

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Met Lys Phe Phe Val Phe Ala Leu Val Leu Ala Leu Met Ile Ser Met
          -15          -10          -5
Ile Ser Ala Asp Ser His Glu Lys Arg His His Gly Tyr Arg Arg Lys
          1          5          10
Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
          15          20          25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
30          35          40          45
Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
          50          55

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          Met Arg Leu Pro Ala Gln Leu
          -15
ctg ggg ctg cta atg ctc tgg gtc tct gga tcc agt ggg gat att gtg 100
Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val

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ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcagg 730

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 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15

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atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
                20                25                30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
                35                40                45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
                50                55                60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
                65                70                75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80                85                90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcaggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<210> 12
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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
                20                25                30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35                40                45                50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
                55                60                65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
                70                75                80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcggggac ccacagcctg 180
gccctcagggc ctgaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
      Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
            -10                    -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
      1              5              10              15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
            20              25              30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
            35              40              45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
            50              55              60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
            65              70              75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80              85              90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt attatccaca ttttgcagat gaggaacag agtcaggtga 694
agtgtctttt ccaaggccaa gctcctgagg gcaggggc 732

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<210> 14
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
      5              10              15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20              25              30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35              40              45              50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
            55              60              65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
            70              75              80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      85              90

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<210> 15
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 <212> DNA
 <213> Homo sapiens

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 <222> 254..574

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 <222> 575..733

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

<210> 16
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..14

<400> 16
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 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 17

<211> 1175
 <212> DNA
 <213> Homo sapiens

<220>
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 <221> CDS
 <222> 327..1013

<220>
 <221> 3'UTR
 <222> 1014..1175

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 <222> 1131..1136

<220>
 <221> polyA_site
 <222> 1160..1175

<400> 17
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 aacccttcg agcaagacgt ggtgatgcc aattggtggaa aggagaaaat cacagaggaa 180
 taggactttt cccatccaat tttgtaacaa ctaatttaaa catagagact gaggcagcgg 240
 ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
 agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353
 Met Asp Arg Ala Leu Gln Val Leu Gln
 1 5
 agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat 401
 Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
 10 15 20 25
 tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449
 Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
 30 35 40
 gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497
 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
 45 50 55
 gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
 60 65 70
 gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593
 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
 75 80 85
 gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
 90 95 100 105
 gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
 110 115 120
 tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737
 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
 125 130 135
 aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
 140 145 150
 agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833
 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
 155 160 165

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tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg      881
Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
170                               175          180          185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg      929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
                               190          195          200
cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca      977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
                               205          210          215
cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa      1023
Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
                               220          225
tcaagcattt tcttgaaagc cttcataagt gtattattca gtccttgtga taccaacctg 1083
aaaatattaa aacttttttc cctctcaact caaaaggacc atgaataaat aaagcacaaa 1143
aacctctctt attctgaaaa aaaaaaaaaa at                                1175

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<210> 18

<211> 229

<212> PRT

<213> Homo sapiens

<400> 18

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Met Asp Arg Ala Leu Gln Val Leu Gln Ser Ile Asp Pro Thr Asp Ser
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Lys Pro Asp Ser Gln Asp Leu Leu Asp Leu Glu Asp Ile Cys Gln Gln
                               20          25          30
Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
                               35          40          45
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
                               50          55          60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
65                               70          75          80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
                               85          90          95
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
                               100          105          110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
                               115          120          125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
130                               135          140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
145                               150          155          160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
                               165          170          175
Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
                               180          185          190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
                               195          200          205
Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
210                               215          220
Gln Gln Pro Leu Leu
225

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<210> 19

<211> 844

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..111

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<221> CDS
 <222> 112..813

<220>
 <221> 3'UTR
 <222> 814..844

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 Met Arg
 -15
 gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165
 Ala Trp Ile Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
 -10 -5 1
 cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
 Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
 5 10 15
 gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261
 Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val
 20 25 30
 gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309
 Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val
 35 40 45 50
 gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357
 Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val
 55 60 65
 tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405
 Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro
 70 75 80
 acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453
 Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn
 85 90 95
 gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501
 Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys
 100 105 110
 acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549
 Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile
 115 120 125 130
 ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597
 Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu
 135 140 145
 ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645
 Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu
 150 155 160
 tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693
 Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu
 165 170 175
 cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741
 Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp
 180 185 190
 cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789
 His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg
 195 200 205 210
 aag gcc aaa atc aag agt gag atg tagaaagttg taaaatagaa aaagtggagt 843
 Lys Ala Lys Ile Lys Ser Glu Met
 215
 t 844

<210> 20
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

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 1 5 10 15
 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
 20 25 30
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
 35 40 45
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
 50 55 60
 Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
 65 70 75
 Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys
 80 85 90 95
 Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr
 100 105 110
 Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp
 115 120 125
 Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu
 130 135 140
 Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val
 145 150 155
 Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln
 160 165 170 175
 Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala
 180 185 190
 Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser
 195 200 205
 Ala Arg Lys Ala Lys Ile Lys Ser Glu Met
 210 215

<210> 21
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..126

<220>
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 <222> 127..1020

<220>
 <221> 3'UTR
 <222> 1021..1997

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 gagttttgtc ccacagtcag caggccacta gtattattaac ttccagtcac cttgattttt 120
 gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg 168
 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val
 -15 -10 -5
 cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
 1 5 10

tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt agc caa gat	264
Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp	
15 20 25	
tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act	312
Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr	
30 35 40	
gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca	360
Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala	
45 50 55 60	
ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt	408
Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys	
65 70 75	
ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac	456
Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp	
80 85 90	
att gat gct gta cca ccc tta cca aag gaa tca gcc tat ctt tac gca	504
Ile Asp Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala	
95 100 105	
cga ttc aac aaa att aaa aag ctg act gcc aaa gat ttt gca gac ata	552
Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile	
110 115 120	
cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata	600
Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile	
125 130 135 140	
gaa gat ggt act ttt tca aaa ctt tct ctg tta gaa gaa ctt tca ctt	648
Glu Asp Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu	
145 150 155	
gct gaa aat caa cta cta aaa ctt cca gtt ctt cct ccc aag ctc act	696
Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr	
160 165 170	
tta ttt aat gca aaa tac aac aaa atc aag agt agg gga atc aaa gca	744
Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala	
175 180 185	
aat gca ttc aaa aaa ctg aat aac ctc acc ttc ctc tac ttg gac cat	792
Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His	
190 195 200	
aat gcc ctg gaa tcc gtg cct ctt aat tta cca gaa agt cta cgt gta	840
Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val	
205 210 215 220	
att cat ctt cag ttc aac aac ata gct tca att aca gat gac aca ttc	888
Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe	
225 230 235	
tgc aag gct aat gac acc agt tac atc cgg gac cgc att gaa gag ata	936
Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile	
240 245 250	
cgc ctg gag ggc aat cca atc gtc ctg gga aag cat cca aac agt ttt	984
Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe	
255 260 265	
att tgc tta aaa aga tta ccg ata ggg tca tac ttt taacctctat	1030
Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe	
270 275 280	
tggtacaaca tataaatgaa agtacaccta cactaatagt ctgtctcaac aatgagtaaa	1090
ggaacttaag tattgggtta atattaacct tgtatctcat tttgaaggaa tttaatat	1150
taagcaagga tgttcaaaat cttacatata ataagtaaaa agtaagactg aatgtctacg	1210
ttcgaaacaa agtaatatga aaatatatta acagcattac aaaatcctag tttatactag	1270
actaccat	1330
ttactaatga tgtaagtacg aggataaatc caagaaactt tcaactcttt gcctttcctg	1390
gccttttactg gatcccaaaa gcatttaagg tacatgttcc aaaaactttg aaaaagctaaa	1450
tgtttcccat gatcgctcat tcttctttta tgattcatac gttattcctt ataaagtaag	1510
aactttggtt tcttctatc aaggcagcta ttttattaaa tttttcactt agtctgagaa	1570
atagcagata gtctcatatt taggaaaact ttccaaataa aataaatgtt attctctgat	1630
aaagagctaa tacagaaatg ttcaagttat tttactttct ggtaatgtct tcagtaaaat	1690
attttcttta tctaaatatt aacattctaa gtctaccaaa aaaagt	1750

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ggccaaaacc aatatgctta taagaaataa tgaaaagttc atccatttct gataaagttc 1810
tctatggcaa agtctttcaa atacgagata actgcaaaat attttccttt tatactacag 1870
aaatgagaat ctcataata aattagttca agcataagat gaaaacagaa tattctgtgg 1930
tgccagtgc cactaccttc ccaccatac acatccatgt tcactgtaac aaactgaata 1990
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1997

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<210> 22
<211> 298
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..19

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<400> 22
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Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile Tyr Asp
1 5 10
Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
15 20 25
Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
30 35 40 45
Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
50 55 60
Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
65 70 75
Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp
80 85 90
Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
95 100 105
Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
110 115 120 125
Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp
130 135 140
Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
145 150 155
Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
160 165 170
Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
175 180 185
Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
190 195 200 205
Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
210 215 220
Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
225 230 235
Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
240 245 250
Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys
255 260 265
Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
270 275

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<210> 23
<211> 1746
<212> DNA
<213> Homo sapiens

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<220>
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<222> 1..9

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<220>
 <221> CDS
 <222> 10..1212

 <220>
 <221> 3'UTR
 <222> 1213..1746

 <220>
 <221> polyA_signal
 <222> 1709..1714

 <220>
 <221> polyA_site
 <222> 1733..1746

<400> 23
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 Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
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 tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
 Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
 1 5 10
 ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
 Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
 15 20 25 30
 agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
 Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
 35 40 45
 atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
 Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
 50 55 60
 atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
 Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
 65 70 75
 gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
 Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
 80 85 90
 ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
 Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
 95 100 105 110
 gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
 Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
 115 120 125
 tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
 Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
 130 135 140
 tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
 Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
 145 150 155
 aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579
 Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
 160 165 170
 ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627
 Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
 175 180 185 190
 aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675
 Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
 195 200 205
 tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg 723
 Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
 210 215 220

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aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac 771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
225 230 235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
240 245 250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
255 260 265 270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc 915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
275 280 285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc 963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
290 295 300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct 1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
305 310 315
ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca 1059
Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
320 325 330
gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
335 340 345 350
gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc 1155
Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
355 360 365
ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
370 375 380
ctg ctg aag tgaggaggcc catgggcaga agatagggat tcccctggac 1252
Leu Leu Lys
385
cacacctcgc tgggttcactt tggtcacaag taggagacac agatggcacc tgtggccaga 1312
gcacctcagg accctcccca cccaccaaag gcctctgcct tgatggagaa ggaaaaggct 1372
ggcaagggtgg gttccaggga ctgtacctgt aggagacaga aaagagaaga aagaagcact 1432
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acttcagccc tgaacctttg tcaccattcc tttaaattct ccaacccaaa gtattcttct 1552
tttcttagtt tcagaagtac tggcatcaca cgcagggttac cttggcgtgt gtccctgtgg 1612
taccctggca gagaagagac caagcttggt tcctgtgtgg ccaaagtcag taggagagga 1672
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aaaaaaaaaaaa 1746

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 <212> PRT
 <213> Homo sapiens

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 <222> 1..17

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 1 5 10 15
 Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
 20 25 30
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
 35 40 45
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 50 55 60

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
 65 70 75
 Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
 80 85 90 95
 Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
 100 105 110
 Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
 115 120 125
 Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
 130 135 140
 Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
 145 150 155
 Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
 160 165 170 175
 Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
 180 185 190
 Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
 195 200 205
 Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
 210 215 220
 Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
 225 230 235
 Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
 240 245 250 255
 Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
 260 265 270
 Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
 275 280 285
 Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
 290 295 300
 His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val
 305 310 315
 Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
 320 325 330 335
 Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu
 340 345 350
 Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg
 355 360 365
 Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu
 370 375 380
 Lys

<210> 25
 <211> 1239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..126

<220>
 <221> CDS
 <222> 127..879

<220>
 <221> 3'UTR
 <222> 880..1239

<220>
 <221> polyA_site
 <222> 1224..1239

<220>

<221> SIGNAL

<222> 1..24

<400> 26

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-20 -15 -10
Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
-5 1 5
Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
10 15 20
Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
25 30 35 40
Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
45 50 55
Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
60 65 70
Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
75 80 85
Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
90 95 100
Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
105 110 115 120
Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
125 130 135
Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
140 145 150
His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
155 160 165
Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
170 175 180
Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
185 190 195 200
Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
205 210 215
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
220 225

<210> 27

<211> 1179

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..115

<220>

<221> CDS

<222> 116..961

<220>

<221> 3'UTR

<222> 962..1179

<220>

<221> polyA_signal

<222> 1145..1150

<220>

<221> polyA_site

<222> 1164..1179

<210> 28
 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28
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 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
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 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

<210> 29
 <211> 1118
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..344

<220>
 <221> CDS
 <222> 345..1118

<220>
 <221> polyA_site
 <222> 1103..1118

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 tgtggcctgg ggaaggagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
 tgggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
 aacccttggg gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
 cgccccgcag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
 Met Gly Arg Thr
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
 -15 -10 -5 1
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
 5 10 15
 atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
 20 25 30
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
 Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
 35 40 45
 aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
 50 55 60 65
 gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
 Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
 70 75 80
 gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
 Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
 85 90 95
 gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
 Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
 100 105 110
 tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
 Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
 115 120 125
 ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
 Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
 130 135 140 145
 gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
 Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
 150 155 160
 cca gct aca aca tgg cct gtc ccg aga ggc aag ttc aac ttt cct tat 932
 Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
 165 170 175
 aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
 Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
 180 185 190
 atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
 Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
 195 200 205
 act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
 Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
 210 215 220 225
 gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa 1118
 Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys

<210> 30
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>
 <221> UNSURE
 <222> 49
 <223> Xaa = Glu, *

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 -20 -15 -10 -5
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 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..13

<220>
 <221> CDS
 <222> 14..1048

<220>
 <221> 3'UTR
 <222> 1049..1273

<220>
 <221> polyA_signal
 <222> 1234..1239

<220>
 <221> polyA_site
 <222> 1258..1273

<400> 31
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 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
 -25 -20 -15
 tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag 97
 Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
 -10 -5 1
 ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac 145
 Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
 5 10 15
 ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt 193
 Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val
 20 25 30 35
 gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga 241
 Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg
 40 45 50
 agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc 289
 Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro
 55 60 65
 tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt 337
 Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe
 70 75 80
 aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg 385
 Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu
 85 90 95
 aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg 433
 Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu
 100 105 110 115
 gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac 481
 Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn
 120 125 130
 aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att 529
 Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
 135 140 145
 ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg 577
 Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
 150 155 160
 cag cgg aca atg atc aga tat ttc aca tcg aat cca gcc tca aag gtc 625
 Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
 165 170 175
 ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt 673
 Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
 180 185 190 195
 cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata 721
 His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
 200 205 210
 gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca 769
 Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala
 215 220 225
 ggt gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga 817

Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly
230 235 240
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg 865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met
245 250 255
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca 913
Asp Thr Ala Gly Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala
260 265 270 275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat 961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His
280 285 290
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa 1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
295 300 305
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg 1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys
310 315 320
attggacagt agtgggtgcat ctgggtccttg ccgcctgaga gccccaggag acatcggcta 1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc 1178
agctgtgtcc cccagtccgt gtcttttttag aatgtgaatg atgataaagt tgtgaaataa 1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaa 1273

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<211> 345
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..26

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Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
-10 -5 1 5
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
10 15 20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
25 30 35
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
40 45 50
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
55 60 65 70
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
75 80 85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
90 95 100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
105 110 115
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
120 125 130
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
135 140 145 150
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
155 160 165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
170 175 180
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
185 190 195
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
200 205 210
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser

215 220 225 230
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 235 240 245
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 250 255 260
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
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 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447

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Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
110          115          120          125
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
          130          135          140
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
          145          150          155
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
          160          165          170
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
          175          180          185
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
190          195          200
aagatgtgtt aaaataaaaa aaaaaaaaaa t 723

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<210> 34
<211> 200
<212> PRT
<213> Homo sapiens

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<400> 34
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
1          5          10          15
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
          20          25          30
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
          35          40          45
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
          50          55          60
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
          65          70          75          80
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
          85          90          95
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
          100          105          110
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
          115          120          125
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
          130          135          140
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
          145          150          155          160
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
          165          170          175
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
          180          185          190
Asp Cys Asp Cys Glu Gln Cys Cys
          195          200

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<210> 35
<211> 845
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..118

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<220>
<221> CDS

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<222> 119..655

<220>

<221> 3'UTR

<222> 656..845

<220>

<221> polyA_signal

<222> 809..814

<220>

<221> polyA_site

<222> 830..845

<400> 35

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acaaatagcc ccgatatct gtgttaccag ccttgtctcg gccacctcaa ggataatcac 60
taaattctgc caaaaggact gaggaacggt gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggt 755
attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815
cagtttatta tcgcaaaaaa aaaaaaaaaa 845
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<210> 36

<211> 179

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe

1 5 10 15
 Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
 20 25 30
 Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
 35 40 45
 Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
 50 55 60
 Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
 65 70 75 80
 Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
 85 90 95
 Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
 100 105 110
 Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
 115 120 125
 Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
 130 135 140
 Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
 145 150 155 160
 Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
 165 170 175

Gly Pro Tyr

<210> 37

<211> 517

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..16

<220>

<221> CDS

<222> 17..259

<220>

<221> 3'UTR

<222> 260..517

<400> 37

ttccatagaa tgggag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52
 Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu

 1 5 10
 gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
 Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu

 15 20 25
 gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
 Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu

 30 35 40
 gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
 Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser

 45 50 55 60
 aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
 Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp

 65 70 75
 gga caa gaa ata gcc tgacatgag gaccagggag ctgctacccc tccctacagc 299
 Gly Gln Glu Ile Ala

 80
 tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcatcct 359
 gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419

tttctccaat ggacatgatt cccaagtcat cctgctgcct tttttcttat agacacaatg 479
 aacagaccac ccacaacctt agttctctaa gtcacccct 517

<210> 38
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
 1 5 10 15
 Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
 20 25 30
 Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Asn Ala
 35 40 45
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
 50 55 60
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 65 70 75 80
 Ala

<210> 39
 <211> 1816
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..259

<220>
 <221> CDS
 <222> 260..1048

<220>
 <221> 3'UTR
 <222> 1049..1816

<220>
 <221> polyA_signal
 <222> 1782..1787

<220>
 <221> polyA_site
 <222> 1801..1816

<400> 39
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 ggaacctcgg gagcggcagc tccggcgccct ggtagcgaga ggcgggttcc ggagatcccg 120
 gcctcacttc gtccactgt ggtaggggt ggtcctgcg aatgttaagt gatttgctca 180
 aggtgcccat ttgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
 -15 -10
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
 10 15 20
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
 25 30 35 40
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg ccc 484
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro

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      45      50      55
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
      60      70
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
      75      80      85
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
      90      95      100
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc 676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
      105      110      115      120
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
      125      130      135
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
      140      145      150
att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc 820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
      155      160      165
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc 868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
      170      175      180
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
      185      190      195      200
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
      205      210      215
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
      220      225      230
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgctc 1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
      235      240
tcccaagaac agagcctgtc cccagatgtc ccagtagcga tgagtaacag aggtggctgt 1118
ggacttcctc tacttctcct tgctggatca gggccttctc gcctcccgtc gggcaggtct 1178
ggccttgcctc tcttggcagg gccccagccc ctctgaccac tctgcagctc accatgcagc 1238
tgatgccaaa gttgtggtgt ccagtgtgca gcagccctgg gagccactgc caccttcaga 1298
ggggttcctt gctgagaccc acattgcttc acctggcccc accatggctg cttgcctggc 1358
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atagggtgga gagcgggaag ggtcttgcct ctaagtgttg ctgctgtggc ttttttgctc 1478
tctccaaaga cgcactgcca ggtcccaagc ttcagactgc tgtgcttagt aagcaagtga 1538
gaagcctggg gtttgagacc cacctactct ctggcagcat cagcatccta ctctggcaa 1598
catcaggcca acgtccaccc cagcctcaca ctgcagatg ttggcagaag ggctaattat 1658
gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cacctgggtc 1718
ccatgaccag ctccccgtct ccataggggt aggcatttca ctggtttatg aagctcgagt 1778
ttcattaaat atgttaagaa tcaaaaaaaaa aaaaaaaaa 1816

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<210> 40
 <211> 263
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<400> 40
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu Leu Leu Gly Ser Leu
 -20 -15 -10 -5

Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys
 45 50 55 60
 Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
 65 70 75
 Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
 80 85 90
 Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
 95 100 105
 Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
 110 115 120
 Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
 125 130 135 140
 Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
 145 150 155
 Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
 160 165 170
 Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
 175 180 185
 Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
 190 195 200
 Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
 205 210 215 220
 Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
 225 230 235
 Arg Gln Pro Tyr Lys Ser Trp
 240

<210> 41
 <211> 643
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..90

<220>
 <221> CDS
 <222> 91..462

<220>
 <221> 3'UTR
 <222> 463..643

<220>
 <221> polyA_signal
 <222> 607..612

<220>
 <221> polyA_site
 <222> 628..643

<400> 41
 acccctaccc cacgccccct cccgcgcgcg cggttaaatc cccgcacctg agcatcggct 60
 cacacctgca ccccgccccg gcatagcacc atg cct gct tgt cgc cta ggc ccg 114
 Met Pro Ala Cys Arg Leu Gly Pro


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cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162
Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
-20 -15 -10
gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
-5 1 5 10
gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala
15 20 25
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu
30 35 40
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro
45 50 55
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro
60 65 70 75
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val
80 85 90
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502
Thr Pro Asn Phe
95
agttttctgcc tggccctgca tctgggtcca gcccacctgc cctcccccttt ttcgggactc 562
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622
tcagcaaaaaa aaaaaaaaaa a 643

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<210> 42
<211> 124
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..30

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<400> 42
Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser
-30 -25 -20 -15
Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys
-10 -5 1
Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu
5 10 15
Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala
20 25 30
Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys
35 40 45 50
Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln
55 60 65
Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn
70 75 80
Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe
85 90

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<210> 43
<211> 501
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..227

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<220>
 <221> CDS
 <222> 228..501

<400> 43
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 agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
 ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
 Met Gln Gly
 -30
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
 Thr Pro Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
 -25 -20 -15
 aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
 -10 -5 1
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
 Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
 5 10 15
 cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
 Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
 20 25 30 35
 gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
 Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
 40 45 50
 gtt cct ttc tcc gaa ctg aaa gac a 501
 Val Pro Phe Ser Glu Leu Lys Asp
 55

<210> 44
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..33

<400> 44
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 -30 -25 -20
 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
 -15 -10 -5
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
 1 5 10 15
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
 20 25 30
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
 35 40 45
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
 50 55

<210> 45
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..97

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 35 40 45
 Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
 50 55 60
 Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
 65 70 75 80
 Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
 85 90 95
 Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
 100 105 110
 Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
 115 120 125
 Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
 130 135 140
 Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys
 145 150 155 160
 Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
 165 170 175
 Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
 180 185 190
 Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
 195 200 205
 Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
 210 215 220
 Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
 225 230 235 240
 Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
 245 250 255
 Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
 260 265 270
 Trp Gly Trp Gly Gln Gly Phe
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 ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
 ttcaataacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
 gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
 Met Ile Tyr Thr Met Lys Lys Val His
 -25 -20
 gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
 Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25 30
 gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
 Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 35 40 45
 att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
 Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
 80 85 90
 cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
 Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
 95 100 105 110
 gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
 Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
 115 120 125
 aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
 Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
 130 135 140
 cag gtg gat aat tat gga acc cag ctg aat gct gtg aat aac tcc ctg 821
 Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
 145 150 155
 act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
 Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
 160 165 170
 tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
 Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
 175 180 185 190
 aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
 Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
 195 200 205
 tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
 Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
 210 215 220
 tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061

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ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
Gly Leu Ile Lys Thr Lys Arg Lys Lys Arg Lys Gln Arg Val Lys Ile
      240              245              250
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt 1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
      255              260
aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tatttttctt 1219
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aaaaaaaaaa aaaaaa 1294

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      -10              -5              1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
      5              10              15              20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
      25              30              35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
      40              45              50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
      55              60              65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
      70              75              80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
      85              90              95              100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
      105              110              115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
      120              125              130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
      135              140              145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
      150              155              160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
      165              170              175              180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
      185              190              195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
      200              205              210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
      215              220              225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
      230              235              240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
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Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20                               -15          -10          -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag      152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
                               1              5              10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa      200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
                               15              20              25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc      248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
                               30              35              40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta      296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
                               45              50              55              60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc      344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
                               65              70              75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac      392
Phe Thr Val Asn Phe Gly Asp Thr Glu Ala Lys Lys Gln Ile Asn
                               80              85              90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag      440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
                               95              100             105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt      488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
                               110             115             120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag      536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
                               125             130             135             140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag      584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
                               145             150             155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg      632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
                               160             165             170
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Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
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175	180	185	
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Pro Asp Glu Gly Lys Leu	Gln His Leu Glu Asn	Glu Leu Thr His Asp	
190	195	200	
atc atc acc aag ttc ctg	gaa aat gaa gac aga	agg tct gcc agc tta	776
Ile Ile Thr Lys Phe Leu	Glu Asn Glu Asp Arg	Arg Ser Ala Ser Leu	
205	210	215	220
cat tta ccc aaa ctg tcc	att act gga acc tat	gat ctg aag agc gtc	824
His Leu Pro Lys Leu Ser	Ile Thr Gly Thr Tyr	Asp Leu Lys Ser Val	
225	230	235	
ctg ggt caa ctg ggc atc	act aag gtc ttc agc	aat ggg gct gac ctc	872
Leu Gly Gln Leu Gly Ile	Thr Lys Val Phe Ser	Asn Gly Ala Asp Leu	
240	245	250	
tcc ggg gtc aca gag gag	gca ccc ctg aag ctc	tcc aag gcc gtg cat	920
Ser Gly Val Thr Glu Glu	Ala Pro Leu Lys Leu	Ser Lys Ala Val His	
255	260	265	
aag gct gtg ctg acc atc	gac gag aaa ggg act	gaa gct gct ggg gcc	968
Lys Ala Val Leu Thr Ile	Asp Glu Lys Gly Thr	Glu Ala Ala Gly Ala	
270	275	280	
atg ttt tta gag gcc ata	ccc atg tct atc ccc	ccc gag gtc aag ttc	1016
Met Phe Leu Glu Ala Ile	Pro Met Ser Ile Pro	Pro Glu Val Lys Phe	
285	290	295	300
aac aaa ccc ttt gtc ttc	tta atg att gac caa	aat acc aag tct ccc	1064
Asn Lys Pro Phe Val Phe	Leu Met Ile Asp Gln	Asn Thr Lys Ser Pro	
305	310	315	
ctc ttc atg gga aaa gtg	gtg aat ccc acc caa	aaa taactgcctc	1110
Leu Phe Met Gly Lys Val	Val Asn Pro Thr Gln	Lys	
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				-5				1				5			
Ile	Leu	Glu	Gly	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro	Glu	Ala	Gln
	10				15					20					
Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn	Gln	Pro	Asp
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Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu	Ser	Glu	Gly
				45				50						55	
Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys	Leu	Tyr	His
			60				65					70			
Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu	Ala	Lys	Lys
		75				80						85			
Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys	Ile	Val	Asp
	90					95				100					
Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu	Val	Asn	Tyr
105					110					115				120	
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp	Thr
				125				130						135	
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Val	Thr	Thr	Val	Lys	Val	Pro
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		155					160					165			
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala	Ile
		170					175				180				
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu	Leu
185					190					195					200
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser
			205						210					215	
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu
			220					225						230	
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly
		235					240					245			
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys
	250					255					260				
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala
265					270					275					280
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu
			285					290						295	
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Asp	Gln	Asn	Thr
			300					305					310		
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys	
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 cgacttttagg ctggataata gtcaaattct tacctcgctc tttcactgct agtaagatca 120
 gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
 aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240
 ccggttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298
 Met Ile Tyr
 -25
 aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
 Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu
 -20 -15 -10
 aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa 394
 Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu
 -5 1 5
 cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442

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His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His
10 15 20
tca ttt tgt gca ttc aag tcg gat gat ggc cca tgt aaa gca atc atg 490
Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met
25 30 35 40
aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata 538
Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile
45 50 55
tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag 586
Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu
60 65 70
tgc aaa aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa 634
Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu
75 80 85
gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac 682
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
90 95 100
aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga tgc ctg ggc 730
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
105 110 115
aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa 778
Asn Met Asn Asn Phe Glu Thr Leu Glu Cys Lys Asn Ile Cys Glu
120 125 130 135
gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctc aat 826
Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn
140 145 150
gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt 874
Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu
155 160 165
ttt gaa ttt cac ggt ccc tca tgg tgt ctc act cca gca gac aga gga 922
Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly
170 175 180
ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg 970
Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly
185 190 195 200
aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat 1018
Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn
205 210 215
ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc 1066
Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile
220 225 230
caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aaa aga aag 1114
Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys
235 240 245
aag cag aga gtg aaa ata gca tat gaa gaa att ttt gtt aaa aat atg 1162
Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
250 255 260
tgaatttgtt atagcaatgt aacattaatt ctactaaata ttttatatga aatgtttcac 1222
tatgattttc tatttttctt ctaaaaatgct tttaattaat atgttcatta aattttctat 1282
gcttattgta cttgttatca aaaaaaaaaa aaaaa 1317

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<210> 52
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 52
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 -25 -20 -15

Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
 40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
 70 75 80
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
 85 90 95 100
 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
 105 110 115
 Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
 120 125 130
 Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
 135 140 145
 Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
 150 155 160
 Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
 165 170 175 180
 Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
 185 190 195
 Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
 200 205 210
 Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
 215 220 225
 Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
 230 235 240
 Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
 245 250 255 260
 Lys Asn Met

<210> 53
 <211> 1907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..1043

<220>
 <221> CDS
 <222> 1044..1664

<220>
 <221> 3'UTR
 <222> 1665..1907

<220>
 <221> polyA_signal
 <222> 1869..1874

<220>
 <221> polyA_site
 <222> 1892..1907

<400> 53
 caaaaaaatt ctagggtcatg atccccataa atgaagagtg atcagtccaa tcccaggga 60

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cctggacatt ttgggtattg tttcagtggg acatgccttt cataagttcc attttcttgg 120
gtatctctta ggaagcaagc ataggaaaca ggcccatccg tctgcctggt ttgcttcttc 180
atctcacttc tacacgaggg tgectgtgct caattgctgt tttcccctaa agagactctt 240
ttccataagt ttgtgaaatg ccatcgacaa acctgatcgc attgcatttc actctgctgt 300
tgagtcgatt tttctttatt ttatcattta gtaactcctt gctctacaga gctttcacct 360
tccacatatt tcagattcat tctttcctaa actatgtggg ggctctacgc ctactgact 420
tatcaacatg ctaccatcat gcacttctta tctctattcc tcttctttaa atttggttcc 480
aaatggctca caccattatt ctgagctatt acctgcctac gcagtcctag aaagtaagt 540
attcagggaaa cattcccaa aagtaaagtt tctcaggtaa gatcagaaga ctcccatgag 600
tactgtctgc tcaggatcac atctggctcc ttgaagagtg attcatcaga ccttacatag 660
atcttgtcat aaaaatgaaa gaggcctcgg gggaaggtct tgggctggtg gcttctgttg 720
gagtcctggg ctgtgggggtg aaagccgtgg ctgtagagct tcatgaggag ttacttagct 780
ttgctctcct gtggacaggc catgcctgtg cctcccccga gcacgggaaa aattggcata 840
gatggggcct tctcaaaaat cccactcctg gagcactggc caaaattact accatcctga 900
tgctgggctt gcagtccttt cctttgggaa tatgaacatg gtcaaaatta agtgaacgtg 960
tctttctggc tttctgtaca atggagcaga acaaagtatc aatttaacta aaatttgaac 1020
taaactcctt ttccagggtt gga atg cac ttc tgt gga ggc acc ttg ata tcc 1073
Met His Phe Cys Gly Gly Thr Leu Ile Ser
1 5 10
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg
15 20 25
cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu
30 35 40
gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc 1217
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro
45 50 55
aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc 1265
Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile
60 65 70
act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc 1313
Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val
75 80 85 90
gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt 1361
Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly
95 100 105
act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag 1409
Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu
110 115 120
aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc 1457
Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser
125 130 135
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag 1505
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln
140 145 150
ggg gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att 1553
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile
155 160 165 170
tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag 1601
Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys
175 180 185
cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga 1649
Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly
190 195 200
gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag 1704
Val Met Arg Asn Asn
205
aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764
acactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact 1824
gctggattct gtagtaagggt gacatagcta tgacatttgt taaaaataaa ctctgtactt 1884
aactttgaaa aaaaaaaaaa aaa 1907

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<210> 54
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met His Phe Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr
 1 5 10 15
 Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
 20 25 30
 Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
 35 40 45
 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
 50 55 60
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
 65 70 75 80
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
 85 90 95
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
 100 105 110
 Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
 115 120 125
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
 130 135 140
 His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 145 150 155 160
 Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
 165 170 175
 Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
 180 185 190
 Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 195 200 205

<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..25

<220>
 <221> CDS
 <222> 26..628

<220>
 <221> 3'UTR
 <222> 629..809

<220>
 <221> polyA_signal
 <222> 766..771

<220>
 <221> polyA_site
 <222> 795..809

<400> 55
 agaaagggtgt ggttggcatg gggca atg ctt gag gta tca gat gca ctg gga 52
 Met Leu Glu Val Ser Asp Ala Leu Gly
 1 5
 gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100

Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
10 15 20 25
acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148
Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
30 35 40
aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196
Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro
45 50 55
ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc 244
Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser
60 65 70
ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292
Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val
75 80 85
ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340
Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala
90 95 100 105
tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388
Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala
110 115 120
ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat 436
Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp
125 130 135
ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag 484
Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu
140 145 150
gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tgc gat ctg 532
Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu
155 160 165
gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc 580
Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala
170 175 180 185
aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc 628
Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys
190 195 200
tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaaacccc 688
ctccagcact ggagggagct ggtttgaagt atgactttgt actggggccca cactcacctc 748
tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaaaa aaaaaaaaaa 808
t 809

<210> 56
<211> 201
<212> PRT
<213> Homo sapiens

<400> 56
Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly
1 5 10 15
Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu
20 25 30
Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His
35 40 45
Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Tyr Lys Glu Ala
50 55 60
Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn
65 70 75 80
Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe
85 90 95
Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala
100 105 110
Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn
115 120 125
Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg

130 135 140
 Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr
 145 150 155 160
 Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser
 165 170 175
 Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn
 180 185 190
 Ser Phe Arg Ile His Phe Trp Gly Cys
 195 200

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
 <221> 3'UTR
 <222> 965..1133

<220>
 <221> polyA_signal
 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
 gacataatca gagctatgct ggaggagaag agggcagcca tttgctggct ggcttgcagt 60
 gagccaggag gtggcaggac gagttaggag gctggttcag tagctcgggc aagagcaggg 120
 cccccagga tctgaaggcc tcccaggccc ccaggcccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaaggc cgaccaggga tttcaaggcc agccaggctt 240
 tccgggcccc ccgggtcccc ctggattccc aggcaaagt ggatcacctg gcccacctgg 300
 ccctcaagca gagaaggcca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360
 tgggccaccg ggacctcctg ggattcaggg cccgcgcggg ctggatgggt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggctcctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly

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      85      90      95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
      100      105      110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
      115      120      125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
      130      135      140      145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
      150      155      160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacaggttg tgaatgtttt ttttggtggt gttggtgttt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

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<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

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<400> 58
Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro
1      5      10      15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
      20      25      30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
      35      40      45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
      50      55      60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
      65      70      75      80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
      85      90      95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
      100      105      110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
      115      120      125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
      130      135      140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
      145      150      155      160
Pro Phe Gly

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<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..78

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<220>
<221> CDS
<222> 79..642

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<220>
<221> 3'UTR
<222> 643..838

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<220>
 <221> polyA_signal
 <222> 799..804

<220>
 <221> polyA_site
 <222> 823..838

<400> 59

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aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggctc 60
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
               Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
               1         5         10

aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
               15         20         25

aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
               30         35         40

gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
               45         50         55

gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
               60         65         70         75

gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
               80         85         90

gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
               95         100        105

gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
               110        115        120

cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
               125        130        135

gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
               140        145        150        155

tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
               160        165        170

gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
               175        180        185

aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg cacccaccct 692
Lys
gacctctccc tcagctgtcc tgtgccccgc cctctcccgc acactcagtc ccctgcctg 752
gcgttcctgc cgcagctctg acctggtgct gtcgacctgg catcttaata aamcctgctt 812
atacttcctt aaaaaaaaaa aaaaaa 838
  
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<210> 60
 <211> 188
 <212> PRT
 <213> Homo sapiens

<400> 60

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Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1         5         10        15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
20        25        30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
  
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35 40 45
 Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
 50 55 60
 Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
 65 70 75 80
 Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
 85 90 95
 Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
 100 105 110
 Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
 115 120 125
 Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
 130 135 140
 Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
 145 150 155 160
 Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
 165 170 175
 Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
 180 185

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
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 <222> 765..862

<400> 61
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 tggtgtctgc cttaagacgt gcagcctggg ccgtggtgt cactgcgttc ggaccagac 120
 ccgctgcagg cagcagcagc ccccgcccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr

85	90	95	
gag tac ctg cgc cag agc	gtg ggc aac	gag gcc gag atc tgg ctg ggc	560
Glu Tyr Leu Arg Gln Ser	Val Gly Asn	Glu Ala Glu Ile Trp Leu Gly	
100	105	110	
ctc aac gac atg gcg gcc	gag ggc acc tgg gtg gac atg acc ggc gcc		608
Leu Asn Asp Met Ala Ala	Glu Gly Thr Trp Val Asp Met Thr Gly Ala		
115	120	125	130
cgc atc gcc tac aag aac	tgg gag act gag atc acc gcg caa ccc gat		656
Arg Ile Ala Tyr Lys Asn	Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp		
135	140	145	
ggc ggc aag acc gag aac	tgc gcg gtc ctg tca ggc gcg gcc aac ggc		704
Gly Gly Lys Thr Glu Asn	Cys Ala Val Leu Ser Gly Ala Ala Asn Gly		
150	155	160	
aag tgg ttc gac aag cgc	tgc cgc gat cag ctg ccc tac atc tgc cag		752
Lys Trp Phe Asp Lys Arg	Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln		
165	170	175	
ttc ggg atc gtg tagccggcgg	ggcggggggcc gtggggggcc tggaggaggg		804
Phe Gly Ile Val			
180			
caggagccgc gggaggccgg	gaggagggtg gggaccttgc agcccccatc ctctccgt		862

<210> 62
 <211> 202
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

<400> 62	
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-5	1 5 10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys	
15	20 25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln	
30	35 40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys	
45	50 55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu	
60	65 70 75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser	
80	85 90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu	
95	100 105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp	
110	115 120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu	
125	130 135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu	
140	145 150 155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln	
160	165 170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val	
175	180

<210> 63
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 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> 195..587

<220>
 <221> 3'UTR
 <222> 588..618

<220>
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 <222> 578..583

<220>
 <221> polyA_site
 <222> 604..618

<400> 63
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 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
 ttcgtttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
 -20 -15 -10
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
 -5 1 5
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
 10 15 20
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
 25 30 35
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
 40 45 50 55
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
 60 65 70
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
 75 80 85
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
 90 95 100
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
 Cys Phe Ala Leu Leu Asn Cys
 105 110

<210> 64
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 64
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly

Ser	Arg	Ser	Ser	Ile	Ala	Leu	Pro	Gln	Gly	Ser	Met	Ser	Ser	Ile	Lys	
				65					70					75		
tgt	tta	caa	aca	act	gaa	gaa	cct	cct	tcc	aga	act	gca	gga	gcc	atg	515
Cys	Leu	Gln	Thr	Thr	Glu	Glu	Pro	Pro	Ser	Arg	Thr	Ala	Gly	Ala	Met	
			80					85					90			
atg	caa	ttc	aca	gcc	cct	att	ccc	gga	gct	aca	gga	cct	atc	aag	ctc	563
Met	Gln	Phe	Thr	Ala	Pro	Ile	Pro	Gly	Ala	Thr	Gly	Pro	Ile	Lys	Leu	
		95					100				105					
tct	caa	aaa	acc	att	gtg	caa	act	cta	gga	cct	att	gta	caa	tat	cct	611
Ser	Gln	Lys	Thr	Ile	Val	Gln	Thr	Leu	Gly	Pro	Ile	Val	Gln	Tyr	Pro	
	110					115					120					
gga	tcc	aat	ggg	agg	ata	aac	ata	agc	cag	ctc	acc	tca	gag	gat	ctc	659
Gly	Ser	Asn	Gly	Arg	Ile	Asn	Ile	Ser	Gln	Leu	Thr	Ser	Glu	Asp	Leu	
	125				130				135					140		
act	ggg	gct	aaa	gga	agg	gtc	aca	tct	ggg	cca	cag	ttc	cct	aat	agc	707
Thr	Gly	Ala	Lys	Gly	Arg	Val	Thr	Ser	Gly	Pro	Gln	Phe	Pro	Asn	Ser	
			145					150				155				
cac	cat	gtg	cca	gag	aat	cta	cat	gga	tac	atg	aat	tcc	ctt	tcc	ctt	755
His	His	Val	Pro	Glu	Asn	Leu	His	Gly	Tyr	Met	Asn	Ser	Leu	Ser	Leu	
			160					165				170				
ttc	tcc	cct	gct	tgactccctc	tccttatgt	gtaaacaatt	taaaaatatg									807
Phe	Ser	Pro	Ala													
			175													
atagtgtata	aatgaaaaaa	aaaaaaaaa														836

<210> 66
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 66

Met	Thr	Val	Leu	Glu	Ile	Thr	Leu	Ala	Val	Ile	Leu	Thr	Leu	Leu	Gly	
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Leu	Ala	Ile	Leu	Ala	Ile	Leu	Leu	Thr	Arg	Trp	Ala	Arg	Arg	Lys	Gln	
	-5				1				5					10		
Ser	Glu	Met	Tyr	Ile	Ser	Arg	Tyr	Ser	Ser	Glu	Gln	Ser	Ala	Arg	Leu	
			15					20					25			
Leu	Asp	Tyr	Glu	Asp	Gly	Arg	Gly	Ser	Arg	His	Ala	Tyr	Ser	Thr	Gln	
		30					35					40				
Ser	Glu	Arg	Ser	Lys	Arg	Asp	Tyr	Thr	Pro	Ser	Thr	Asn	Ser	Leu	Ala	
	45						50					55				
Leu	Ser	Arg	Ser	Ser	Ile	Ala	Leu	Pro	Gln	Gly	Ser	Met	Ser	Ser	Ile	
	60				65					70						
Lys	Cys	Leu	Gln	Thr	Thr	Glu	Glu	Pro	Pro	Ser	Arg	Thr	Ala	Gly	Ala	
	75				80				85					90		
Met	Met	Gln	Phe	Thr	Ala	Pro	Ile	Pro	Gly	Ala	Thr	Gly	Pro	Ile	Lys	
			95					100				105				
Leu	Ser	Gln	Lys	Thr	Ile	Val	Gln	Thr	Leu	Gly	Pro	Ile	Val	Gln	Tyr	
		110					115					120				
Pro	Gly	Ser	Asn	Gly	Arg	Ile	Asn	Ile	Ser	Gln	Leu	Thr	Ser	Glu	Asp	
	125					130					135					
Leu	Thr	Gly	Ala	Lys	Gly	Arg	Val	Thr	Ser	Gly	Pro	Gln	Phe	Pro	Asn	
	140					145				150						
Ser	His	His	Val	Pro	Glu	Asn	Leu	His	Gly	Tyr	Met	Asn	Ser	Leu	Ser	
	155				160				165					170		
Leu	Phe	Ser	Pro	Ala												
				175												

<210> 67

<211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

<400> 67
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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggaggggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
 caccaccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
 aatgggaaag ggggggaaac tgattttaca cttaataaat aaaatcctat tagtaactcc 772
 gaaaaaaaa aaaaaaa 789

<210> 68
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 68
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 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 69
 <211> 2556
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..66

<220>
 <221> CDS
 <222> 67..2427

<220>
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 <222> 2428..2556

<220>
 <221> polyA_signal
 <222> 2522..2527

<220>
 <221> polyA_site
 <222> 2541..2556

<400> 69
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 cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
 Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
 -15 -10 -5
 ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
 Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
 1 5 10 15

cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat	204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr	
20 25 30	
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg	252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val	
35 40 45	
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg	300
His Leu Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu	
50 55 60	
tac aat caa gga tct atg aat act tat tct tca gat att cag act caa	348
Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln	
65 70 75	
tgc tac tat caa gga aat att gaa gaa tat cca gat tcc atg gtc aca	396
Cys Tyr Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr	
80 85 90 95	
ctc agc acg tgc tct gga cta aga gga ata ctg caa ttt gaa aat gtt	444
Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val	
100 105 110	
tct tat gga att gag cct ctg gaa tct gca gtt gaa ttt cag cat gtt	492
Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val	
115 120 125	
ctt cac aaa tta aag aat gaa gac aat gat att gca att ttt att gac	540
Leu His Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp	
130 135 140	
aga agc ctg aaa gaa caa cca atg gat gac aac att ttt ata agt gaa	588
Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu	
145 150 155	
aaa tca gaa cca gct gtt cca gat tta ttt cct ctt tat cta gaa atg	636
Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met	
160 165 170 175	
cat att gtg gtg gac aaa act ttg tat gat tac tgg ggc tct gat agc	684
His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser	
180 185 190	
atg ata gta aca aat aaa gtc atc gaa att gtt ggc ctt gca aat tca	732
Met Ile Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser	
195 200 205	
atg ttc acc caa ttt aaa gtt act att gtg ctg tca tca ttg gag tta	780
Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu	
210 215 220	
tgg tca gat gaa aat aag att tct aca gtt ggt gag gca gat gaa tta	828
Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu	
225 230 235	
ttg caa aaa ttt tta gaa tgg aaa caa tct tat ctt aac cta agg cct	876
Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro	
240 245 250 255	
cat gat att gca tat cta cta att tat atg gat tat cct cgt tat ttg	924
His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu	
260 265 270	
gga gca gtg ttt cct gga aca atg tgt att act cgt tat tct gca gga	972
Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly	
275 280 285	
gtc gca ttg tac ccc aag gag ata act ctg gag gca ttt gca gtt att	1020
Val Ala Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile	
290 295 300	
gtc acc cag atg ctg gca ctc agt ctg gga ata tca tat gac gac cca	1068
Val Thr Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro	
305 310 315	
aag aaa tgt caa tgt tca gaa tcc acc tgt ata atg aat cca gaa gtt	1116
Lys Lys Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val	
320 325 330 335	
gtg caa tcc aat ggt gtg aag act ttt agc agt tgc agt ttg agg agc	1164
Val Gln Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser	
340 345 350	

ttt	caa	aat	ttc	att	tca	aat	gtg	ggt	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
			355				360						365			
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
			370				375						380			
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggg	act	gag	gct	caa	tgt	gga	1308
Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
			385				390						395			
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
			400				405						410	415		
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	
			420				425						430			
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
			435				440						445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	act	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
			450				455						460			
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
			465				470						475			
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
			480				485						490	495		
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
			500				505						510			
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	
			515				520						525			
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
			530				535						540			
cga	aag	cct	ttc	cat	caa	gaa	aat	ggt	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
			545				550						555			
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
			560				565						570	575		
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala</												

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gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca 2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro
      690      695      700
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa 2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
      705      710      715
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
      720      725      730      735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
      740      745      750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
      755      760      765
caa agc agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
      770
tcgctaagaa atgaaaattc tgtctttcct tccgtgggtca cagctgaaag aaacaataaa 2527
ttgagtggtgg accaaaaaaaa aaaaaaaaaat 2556

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<210> 70
<211> 787
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..16

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<400> 70
Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
  -15      -10      -5
Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
  1      5      10      15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
  20      25      30
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
  35      40      45
Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
  50      55      60
Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
  65      70      75      80
Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
  85      90      95
Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
  100     105     110
Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
  115     120     125
Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
  130     135     140
Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
  145     150     155     160
Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
  165     170     175
Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
  180     185     190
Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
  195     200     205
Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
  210     215     220
Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
  225     230     235     240

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Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
245 250 255
Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
260 265 270
Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
275 280 285
Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr
290 295 300
Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys
305 310 315 320
Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln
325 330 335
Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln
340 345 350
Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln
355 360 365
Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu
370 375 380
Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala
385 390 395 400
Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys
405 410 415
Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val
420 425 430
Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys
435 440 445
Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly
450 455 460
Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His
465 470 475 480
Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn
485 490 495
Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe
500 505 510
Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp
515 520 525
Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys
530 535 540
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp
545 550 555 560
Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp
565 570 575
Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys
580 585 590
Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His
595 600 605
Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn
610 615 620
Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg
625 630 635 640
Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met
645 650 655
Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu
660 665 670
Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg
675 680 685
Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser
690 695 700
Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
705 710 715 720
Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser
725 730 735
Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu

740 745 750
 Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
 755 760 765
 Ser Ser Asn
 770

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 <222> 8..763

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 <222> 764..1603

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 <222> 1562..1567

<220>
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 <222> 1588..1603

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 Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu
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 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
 1 5 10
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
 15 20 25 30
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
 35 40 45
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
 50 55 60
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
 65 70 75
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
 80 85 90
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His
 95 100 105 110
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
 115 120 125
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
 130 135 140
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529

Leu	Val	Ala	Leu	Gly	Pro	Gly	His	Gly	Leu	Gln	Gly	Pro	His	Xaa	Ala		
		145					150					155					
ctc	ctg	gct	gca	atg	ctt	cgg	ggg	ctg	gca	ggg	ggc	cga	gtc	ctg	gcc	577	
Leu	Leu	Ala	Ala	Met	Leu	Arg	Gly	Leu	Ala	Gly	Gly	Arg	Val	Leu	Ala		
		160				165					170						
ctc	ctg	gag	gag	aac	tcc	aca	ccc	cag	cta	gca	ggg	atc	ctg	gcc	cgg	625	
Leu	Leu	Glu	Glu	Asn	Ser	Thr	Pro	Gln	Leu	Ala	Gly	Ile	Leu	Ala	Arg		
		175			180					185				190			
gtg	ctg	aat	gga	gag	gca	cct	cct	agc	cta	ggc	cct	tcc	tct	gtg	gcc	673	
Val	Leu	Asn	Gly	Glu	Ala	Pro	Pro	Ser	Leu	Gly	Pro	Ser	Ser	Val	Ala		
			195						200					205			
tcc	cca	gag	gac	gtc	cag	gcc	ctg	atg	tac	ctg	aga	ggg	cag	ctg	gag	721	
Ser	Pro	Glu	Asp	Val	Gln	Ala	Leu	Met	Tyr	Leu	Arg	Gly	Gln	Leu	Glu		
		210						215				220					
cct	cag	tgg	aag	atg	ttg	cag	tgc	cat	cct	cac	ctg	gtg	gct			763	
Pro	Gln	Trp	Lys	Met	Leu	Gln	Cys	His	Pro	His	Leu	Val	Ala				
		225				230					235						
tgaaatcggc	caaggtggga	gcattttacac	cgcagaaatg	acaccgcacg	ccagcgcccc	823											
gcgccgcgca	tccggacccc	aagcccacgg	ctccctcgac	tctggggcac	ggaaccccg	883											
ccactcccaa	tccccgcgcc	ccgccctctc	ccaccctgtc	ttcccccgct	ccaccctca	943											
cctcacctcg	ccccgcgcc	acccatcgcg	ccccggcggc	tggtattgtt	cggctgggct	1003											
cggtcggggc	ctgtctccct	cggctctgcg	ggtgtcagtt	cgtccggctt	cctcacagcc	1063											
cctcactccc	ggcggtgac	agcagcagcg	gcggcgcgcg	gcggcgccctg	gcgtttcgag	1123											
gctgagcggc	accgggggtt	gggcgcggag	gaggagcagc	agcgggagga	ggagccgtgt	1183											
gccctggcac	tgagcggccg	cggccatggc	gtacgcctat	ctcttcaagt	acatcataat	1243											
cggcgacaca	ggtgttggt	aatcatgctt	attgctacag	tttacagaca	agaggttcag	1303											
ccagtgcatt	accttactat	tgggtgtagag	ttcgggtgctc	gaatgataac	tattgatggg	1363											
aaacagataa	aacttcagat	atgggatacg	gcagggcaag	aatcctttcg	ttccatcaca	1423											
aggtcgtatt	acagaggtgc	agcaggagct	ttactagttt	acgatattac	acggagagat	1483											
acattcaacc	acttgacaac	ctgggttagaa	gatgcccgcc	agcattccaa	ttccaacatg	1543											
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<210> 72
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<220>
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 <222> 173
 <223> Xaa = Ala,Gly

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		-15				-10				-5							
Leu	Arg	Val	Cys	Val	Ser	Leu	Trp	Ser	Val	His	His	Arg	Pro	His	Glu		
	1			5					10						15		
Ser	Leu	Ala	Arg	Glu	Ala	Leu	Thr	Ala	Leu	Gly	Lys	Leu	Leu	Tyr			
			20					25						30			
Leu	Leu	Asp	Gly	Met	Leu	Asp	Gly	Gln	Val	Asn	Ser	Gly	Ile	Ala	Ala		
		35					40					45					
Thr	Pro	Ala	Ser	Ala	Ala	Ala	Ala	Thr	Leu	Asp	Val	Ala	Val	Arg	Arg		
	50					55					60						
Gly	Leu	Ser	His	Ala	Ala	Gln	Arg	Leu	Leu	Cys	Val	Ala	Leu	Gly	Gln		
	65				70					75							
Leu	Asp	Arg	Pro	Pro	Asp	Leu	Ala	His	Asp	Gly	Arg	Ser	Leu	Trp	Leu		
	80				85				90						95		
Asn	Ile	Arg	Gly	Lys	Glu	Ala	Ala	Ala	Leu	Ser	Met	Phe	His	Val	Ser		
			100					105						110			

Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly
115 120 125
Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val
130 135 140
Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu
145 150 155
Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu
160 165 170 175
Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu
180 185 190
Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro
195 200 205
Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln
210 215 220
Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
225 230 235

<210> 73
<211> 879
<212> DNA
<213> Homo sapiens

<220>
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<222> 1..8

<220>
<221> CDS
<222> 9..395

<220>
<221> 3'UTR
<222> 396..879

<220>
<221> polyA_site
<222> 864..879

<400> 73
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Met Ala Val Leu Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly
-15 -10 -5
cca ggc ccg ggt cct cgg ccg ctg tgg ggc cca ggc ccg gcc tgg agt 98
Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
1 5 10 15
cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
20 25 30
agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194
Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
35 40 45
tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
50 55 60
ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
65 70 75
tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
80 85 90 95
aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
100 105 110

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ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac      435
Ile Phe Ile
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tgggccgggt 495
gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtggtggc 615
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc 675
caacatggtg aaaccccgtc ttactaaaa atagaaaatt agccgggcgt gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaac 855
tccatcccaa aaaaaaaaaa aaaa                                     879

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<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..16

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<400> 74
Met Ala Val Leu Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro Gly
  -15                      -10                      -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
  1                      5                      10                      15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
  20                      25                      30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
  35                      40                      45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
  50                      55                      60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
  65                      70                      75                      80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
  85                      90                      95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
  100                      105                      110
Ile

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<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

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<220>
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<220>
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<220>
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<220>
<221> polyA_site
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<400> 75
aaagttcctc agcccttggc tcctgcccag tgtttagggt gttggcggag acaaagggga 60
agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
10 15 20 25
gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
30 35 40
aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
45 50 55
cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306
Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg
60 65 70
gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354
Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys
75 80 85
ggg tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402
Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val
90 95 100 105
aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450
Lys Glu Ala Glu Val Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln
110 115 120
gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498
Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser
125 130 135
gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546
Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His
140 145 150
gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac 594
Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His
155 160 165
aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642
Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln
170 175 180 185
aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca 690
Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala
190 195 200
cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
205 210 215
gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
220 225 230
cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tgc ggt 834
Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
235 240 245
gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val
250 255 260 265
aag aaa cat aac ttc aca cca ctg gca aga att gtg ggc tac ttt gta 930
Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val
270 275 280
tct gga tgt gat ccc tct atc atg ggt att ggt cct gtc cct gct atc 978
Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile
285 290 295
agt ggg gca ctg aag aaa gca gga ctg agt ctt aag gac atg gat ttg 1026
Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu
300 305 310

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ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
75 80 85 90
aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
95 100 105
aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494
Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
110 115 120
act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc 542
Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
125 130 135
ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg 590
Phe Val Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
140 145 150
aac atg gag gcc gac ccc ggc cag tac cgg tgc aac ggc acc agc tcc 638
Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser
155 160 165 170
aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg 686
Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
175 180 185
gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg 734
Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
190 195 200
gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gac gtc 782
Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
205 210 215
ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag 830
Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
220 225 230
cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc 875
His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
235 240 245
tgaggcaggt ggcccgagga cgtccctgc tccgcgtctg cgccgcggcc ggagtccact 935
cccagtgcct gcaagattcc aagttctcac ctcttaaaga aaaccacccc cgtagattcc 995
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tcaactccaa gccccctcct tgtctgtgca tccgggggca gctctggagg gggtttgtctg 1475
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<210> 78
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 <213> Homo sapiens

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 -20 -15 -10
 His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
 -5 1 5 10
 Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
 15 20 25

tgc	gct	ccc	tgc	cgg	cca	gaa	gag	tgc	gcc	gcg	ccg	cgg	ggc	tgc	ctg	547
Cys	Ala	Pro	Cys	Arg	Pro	Glu	Glu	Cys	Ala	Ala	Pro	Arg	Gly	Cys	Leu	
25						30					35					595
gcg	ggc	agg	gtg	cgc	gac	gcg	tgc	ggc	tgc	tgc	tgg	gaa	tgc	gcc	aac	
Ala	Gly	Arg	Val	Arg	Asp	Ala	Cys	Gly	Cys	Cys	Trp	Glu	Cys	Ala	Asn	643
40					45				50					55		
ctc	gag	ggc	cag	ctc	tgc	gac	ctg	gac	ccc	agt	gct	cac	ttc	tac	ggg	691
Leu	Glu	Gly	Gln	Leu	Cys	Asp	Leu	Asp	Pro	Ser	Ala	His	Phe	Tyr	Gly	
				60					65					70		739
cac	tgc	ggc	gag	cag	ctt	gag	tgc	cgg	ctg	gac	aca	ggc	ggc	gac	ctg	
His	Cys	Gly	Glu	Gln	Leu	Glu	Cys	Arg	Leu	Asp	Thr	Gly	Gly	Asp	Leu	787
			75					80					85			
agc	cgc	gga	gag	gtg	ccg	gaa	cct	ctg	tgt	gcc	tgt	cgt	tcg	cag	agt	835
Ser	Arg	Gly	Glu	Val	Pro	Glu	Pro	Leu	Cys	Ala	Cys	Arg	Ser	Gln	Ser	
		90					95					100				883
ccg	ctc	tgc	ggg	tcc	gac	ggt	cac	acc	tac	tcc	cag	atc	tgc	cgc	ctg	
Pro	Leu	Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Gln	Ile	Cys	Arg	Leu	931
			105			110					115					
cag	gag	gcg	gcc	cgc	gct	cgg	ccc	gat	gcc	aac	ctc	act	gtg	gca	cac	979
Gln	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Asp	Ala	Asn	Leu	Thr	Val	Ala	His	
120					125				130					135		1027
ccg	ggg	ccc	tgc	gaa	tcg	ggg	ccc	cag	atc	gtg	tca	cat	cca	tat	gac	
Pro	Gly	Pro	Cys	Glu	Ser	Gly	Pro	Gln	Ile	Val	Ser	His	Pro	Tyr	Asp	1075
			140					145					150			
act	tgg	aat	gtg	aca	ggg	cag	gat	gtg	atc	ttt	ggc	tgt	gaa	gtg	ttt	1123
Thr	Trp	Asn	Val	Thr	Gly	Gln	Asp	Val	Ile	Phe	Gly	Cys	Glu	Val	Phe	
			155					160					165			1174
gcc	tac	ccc	atg	gcc	tcc	atc	gag	tgg	agg	aag	gat	ggc	ttg	gac	atc	
Ala	Tyr	Pro	Met	Ala	Ser	Ile	Glu	Trp	Arg	Lys	Asp	Gly	Leu	Asp	Ile	1234
		170					175					180				
cag	ctg	cca	ggg	gat	gac	ccc	cac	atc	tct	gtg	cag	ttt	agg	ggg	gga	1294
Gln	Leu	Pro	Gly	Asp	Asp	Pro	His	Ile	Ser	Val	Gln	Phe	Arg	Gly	Gly	
			185			190					195					1354
ccc	cag	agg	ttt	gag	gtg	act	ggc	tgg	ctg	cag	atc	cag	gct	gtg	cgt	
Pro	Gln	Arg	Phe	Glu	Val	Thr	Gly	Trp	Leu	Gln	Ile	Gln	Ala	Val	Arg	1414
200					205				210					215		
ccc	agt	gat	gag	ggc	act	tac	cgc	tgc	ctt	ggc	cca	atg	ccc	tgg	gtc	1466
Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Leu	Gly	Pro	Met	Pro	Trp	Val	
			220					225					230			1294
aag	tgg	agg	ccc	ctg	cta	gct	tgacagt	gct	cacacct	gac						

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<210> 80
<211> 267
<212> PRT
<213> Homo sapiens
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 35 40 45 50
 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
 55 60 65
 His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
 70 75 80
 Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
 85 90 95
 Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
 100 105 110
 Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
 115 120 125 130
 Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
 135 140 145
 His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
 150 155 160
 Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
 165 170 175
 Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
 180 185 190
 Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
 195 200 205 210
 Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
 215 220 225
 Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
 230 235

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

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<220>
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 <222> 27..689

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 <222> 690..1406

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<220>
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<400> 81
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 Met Ala Gly Gly Val Arg Pro Leu Arg
 -30 -25
 ggc ctc cgc gcc ttg tgt cgc gtg ctg ctc ttc ctt tcg cag ttc tgc 101
 Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys
 -20 -15 -10
 att ctg tcg ggc ggt gaa agt act gaa atc cca cct tat gtg atg aag 149

Ile	Leu	Ser	Gly	Gly	Glu	Ser	Thr	Glu	Ile	Pro	Pro	Tyr	Val	Met	Lys	
-5						1				5					10	
tgt	ccg	agc	aat	ggg	ttg	tgt	agc	agg	ctt	cct	gca	gac	tgt	ata	gac	197
Cys	Pro	Ser	Asn	Gly	Leu	Cys	Ser	Arg	Leu	Pro	Ala	Asp	Cys	Ile	Asp	
			15					20						25		
tgc	aca	aca	aat	ttc	tcc	tgt	acc	tat	ggg	aag	cct	gtc	act	ttt	gac	245
Cys	Thr	Thr	Asn	Phe	Ser	Cys	Thr	Tyr	Gly	Lys	Pro	Val	Thr	Phe	Asp	
			30					35					40			
tgt	gca	gtg	aaa	cca	tct	gtt	acc	tgt	gtt	gat	caa	gac	ttc	aaa	tcc	293
Cys	Ala	Val	Lys	Pro	Ser	Val	Thr	Cys	Val	Asp	Gln	Asp	Phe	Lys	Ser	
			45				50					55				
caa	aag	aac	ttc	atc	att	aac	atg	act	tgc	aga	ttt	tgc	tgg	cag	ctt	341
Gln	Lys	Asn	Phe	Ile	Ile	Asn	Met	Thr	Cys	Arg	Phe	Cys	Trp	Gln	Leu	
			60			65					70					
cct	gaa	aca	gat	tac	gag	tgt	acc	aac	tcc	acc	agc	tgc	atg	acg	gtg	389
Pro	Glu	Thr	Asp	Tyr	Glu	Cys	Thr	Asn	Ser	Thr	Ser	Cys	Met	Thr	Val	
75					80				85					90		
tcc	tgt	cct	cgg	cag	cgc	tac	cct	gcc	aac	tgc	acg	gtg	cgg	gac	cac	437
Ser	Cys	Pro	Arg	Gln	Arg	Tyr	Pro	Ala	Asn	Cys	Thr	Val	Arg	Asp	His	
			95					100					105			
gtc	cac	tgc	ttg	ggg	aac	cgt	act	ttt	ccc	aaa	atg	cta	tat	tgc	aat	485
Val	His	Cys	Leu	Gly	Asn	Arg	Thr	Phe	Pro	Lys	Met	Leu	Tyr	Cys	Asn	
			110					115				120				
tgg	act	gga	ggc	tat	aag	tgg	tct	acg	gct	ctg	gct	cta	agc	atc	acc	533
Trp	Thr	Gly	Gly	Tyr	Lys	Trp	Ser	Thr	Ala	Leu	Ala	Leu	Ser	Ile	Thr	
			125				130					135				
ctc	ggg	ggg	ttt	gga	gca	gac	cgt	ttc	tac	ctg	ggc	cag	tgg	cgg	gaa	581
Leu	Gly	Gly	Phe	Gly	Ala	Asp	Arg	Phe	Tyr	Leu	Gly	Gln	Trp	Arg	Glu	
			140			145					150					
ggc	ctc	ggc	aag	ctc	ttc	agc	ttc	ggg	ggc	ctg	gga	ata	tgg	acg	ctg	629
Gly	Leu	Gly	Lys	Leu	Phe	Ser	Phe	Gly	Gly	Leu	Gly	Ile	Trp	Thr	Leu	
155				160						165				170		
ata	gac	gtc	ctg	ctc	att	gga	gtt	ggc	tat	gtt	gga	cca	gca	gat	ggc	677
Ile	Asp	Val	Leu	Leu	Ile	Gly	Val	Gly	Tyr	Val	Gly	Pro	Ala	Asp	Gly	
			175					180					185			
tct	ttg	tac	att	tagctgtggg	gtgtgcttca	gaaaggagca	gggcttagaa									729
Ser	Leu	Tyr	Ile													
			190													
aaagcccttt	tgtccgtagg	agttgatgtg	gtgtgagtga	tatatcttcta	tggttttaaat											789
gtacagcatc	tgtactttgt	ttgccttgat	aaaggtaaga	taaatgaaac	gctgaactat											849
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<210> 82
<211> 221
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 Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 1 5 10 15
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
 20 25 30
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
 35 40 45
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
 50 55 60
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
 65 70 75 80
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
 85 90 95
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
 100 105 110
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
 115 120 125
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
 130 135 140
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
 145 150 155 160
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
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 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
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 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala

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10          15          20          25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          30          35          40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
          75          80          85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
          90          95          100          105
ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
Gly Pro Ser
acagacattc gggagacggc cttcgtgttc gccatcactg cggccgggcgc cagccacgcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggcccctc cccggcccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730
tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
gacgagaagt cgaggctctt tatgsacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
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ctgcctccat ttgcgaggt gggcgcgcg ctgctggagc gcttccacgg cgctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgcg tccgcacgct caagccgcg 1090
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accggtccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
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gagctcagcc tctgcctgtg acccgccgcc cgccgctag actgacttcg cgcagcgggtg 1390
gctcgcacct gtgggacctc agggcacccg caccgggcgc ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccgggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttgccc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggtagg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaa 1754

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<210> 84
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..24

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<400> 84
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
          10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu

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75 80 85
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
 90 95 100
 Gly Pro Ser
 105

<210> 85
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 85
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 gcggttcgcc ccgcagcctc gccccctgcc caccgcggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
 75 80 85
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Phe Gln Val Pro
 90 95 100 105
 ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
 Gly Pro Ser
 acagacattc gggagacggc ctctgtgttc gccatcactg cggcgggcgc cagccacggc 610
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
 cgggcccctc cccggccctc cggcctgccc ggcacccccg gaccccttg ccccgcgggc 730

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tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcgagg ccacacgcgc 910
accgagtgca aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttcgcgaggt gggcgcgcg cgctggagc gcttycacgg cgcctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgccg tccgcacgct caagccgccg 1090
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tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
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aaaa 1754

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```

<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
    10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
    25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
          75          80          85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
    90          95          100
Gly Pro Ser
105

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<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..151

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<220>
<221> CDS
<222> 152..655

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<220>
<221> 3'UTR

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<222> 656..1431

<220>

<221> polyA_signal

<222> 1399..1404

<220>

<221> polyA_site

<222> 1416..1431

<400> 87

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gccccaaacca aggccccccag agagggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1             5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
          10             15             20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
          25             30             35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
          40             45             50             55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
          60             65             70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
          75             80             85
gaa gag gag gat gat gaa gaa gag gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
          90             95             100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
          105             110             115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Glu Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
          120             125             130             135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
          140             145             150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
          155             160             165
aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr
tccccagaaa cccactctat cctcaccctg ttttgtgtctc ttccccctgc ctgctagggc 765
tgcggttctt gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
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gggaacaggg atttgccctt cacaattcta ctccccagat cctctccccct ggacacagga 1005
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acagcggggg gcgcaggtt ttccttgtcc cccagctgct ctgccccctt ccccttcttc 1365
cctgactcca ggccgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431
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<210> 88

<211> 168
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
 1 5 10 15
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 20 25 30
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
 35 40 45
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
 50 55 60
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
 65 70 75 80
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
 85 90 95
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
 100 105 110
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
 115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 89
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 gcccaaacca agggccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120
 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
 Met Leu Phe Arg Leu Ser Glu
 1 5
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
 10 15 20
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268

Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
 25 30 35
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
 40 45 50 55
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
 60 65 70
 ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
 Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
 75 80 85
 gaa gag gag gat gat gaa gaa gag gaa gaa gag gag gac agc cag gct 460
 Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
 90 95 100
 gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
 Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
 105 110 115
 ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
 Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
 120 125 130 135
 tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
 Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
 140 145 150
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
 155 160 165
 aca taggcaccca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
 Thr
 tccccagaaa cccactctat cctcaccctg ttttgtgtctc ttcccctcgc ctgctagggc 765
 tgcggcttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccacacctt 825
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 gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
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 aaaaaa 1431

<210> 90

<211> 168

<212> PRT

<213> Homo sapiens

<400> 90

Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
 1 5 10 15
 Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
 20 25 30
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
 35 40 45
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
 50 55 60
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
 65 70 75 80
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
 85 90 95
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
 100 105 110
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu

115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

<210> 91
 <211> 1417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..47

<220>
 <221> CDS
 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
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 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 65 70 75
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 80 85 90
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 95 100 105
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 110 115 120

ctg Leu 125	aag Lys	cta Leu	gtg Val	gat Asp	aag Lys	ttt Phe	tgt Leu	gag Glu	gat Asp	ggt Val	aaa Lys	aag Lys	tgt Leu	tac Tyr	cac His		536
					130					135					140		
tca Ser	gaa Glu	gcc Ala	ttc Phe	act Thr	gtc Val	aac Asn	ttc Phe	ggg Gly	gac Asp	acc Thr	gaa Glu	gag Glu	gcc Ala	aag Lys	aaa Lys		584
				145					150					155			
cag Gln	atc Ile	aac Asn	gat Asp	tac Tyr	gtg Val	gag Glu	aag Lys	ggt Gly	act Thr	caa Gln	ggg Gly	aaa Lys	att Ile	gtg Val	gat Asp		632
			160					165					170				
ttg Leu	gtc Val	aag Lys	gag Glu	ctt Leu	gac Asp	aga Arg	gac Asp	aca Thr	ggt Val	ttt Phe	gct Ala	ctg Leu	gtg Val	aat Asn	tac Tyr		680
		175					180				185						
atc Ile	ttc Phe	ttt Phe	aaa Lys	ggc Gly	aaa Lys	tgg Trp	gag Glu	aga Arg	ccc Pro	ttt Phe	gaa Glu	gtc Val	aag Lys	gac Asp	acc Thr		728
		190				195				200							
gag Glu 205	gaa Glu	gag Glu	gac Asp	ttc Phe	cac His	gtg Val	gac Asp	cag Gln	gcg Ala	acc Thr	acc Thr	gtg Val	aag Lys	gtg Val	cct Pro		776
				210					215						220		
atg Met	atg Met	aag Lys	cgt Arg	tta Leu	ggc Gly	atg Met	ttt Phe	aac Asn	atc Ile	cag Gln	cac His	tgt Cys	aag Lys	aag Lys	ctg Leu		824
				225				230						235			
tcc Ser	agc Ser	tgg Trp	gtg Val	ctg Leu	ctg Leu	atg Met	aaa Lys	tac Tyr	ctg Leu	ggc Gly	aat Asn	gcc Ala	acc Thr	gcc Ala	atc Ile		872
		240						245				250					
ttc Phe	ttc Phe	ctg Leu	cct Pro	gat Asp	gag Glu	ggg Gly	aaa Lys	cta Leu	cag Gln	cac His	ctg Leu	gaa Glu	aat Asn	gaa Glu	ctc Leu		920
		255				260						265					
acc Thr	cac His	gat Asp	atc Ile	atc Ile	acc Thr	aag Lys	ttc Phe	ctg Leu	gaa Glu	aat Asn	gaa Glu	gac Asp	aga Arg	agg Arg	tct Ser		968
		270				275				280							
gcc Ala 285	agc Ser	tta Leu	cat His	tta Leu	ccc Pro	aaa Lys	ctg Leu	tcc Ser	att Ile	act Thr	gga Gly	acc Thr	tat Tyr	gat Asp	ctg Leu		1016
				290				295						300			
aag Lys	agc Ser	gtc Val	ctg Leu	ggt Gly	caa Gln	ctg Leu	ggc Gly	atc Ile	act Thr	aag Lys	gtc Val	ttc Phe	agc Ser	aat Asn	ggg Gly		1064
				305				310						315			
gct Ala	gac Asp	ctc Leu	tcc Ser	ggg Gly	gtc Val	aca Thr	gag Glu	gag Glu	gca Ala	ccc Pro	ctg Leu	aag Lys	ctc Leu	tcc Ser	aag Lys		1112
			320					325					330				
gcc Ala	gtg Val	cat His	aag Lys	gct Ala	gtg Val	ctg Leu	acc Thr	atc Ile	gac Asp	gag Glu	aaa Lys	ggg Gly	act Thr	gaa Glu	gct Ala		1160
		335				340						345					
gct Ala	ggg Gly	gcc Ala	atg Met	ttt Phe	tta Leu	gag Glu	gcc Ala	ata Ile	ccc Pro	atg Met	tct Ser	atc Ile	ccc Pro	ccc Pro	gag Glu		1208
	350					355					360						
gtc Val 365	aag Lys	ttc Phe	aac Asn	aaa Lys	ccc												

<210> 92

<212> PRT

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<222> 1..24

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<220>
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 <222> 278..733

<220>
 <221> 3'UTR
 <222> 734..1115

<220>
 <221> polyA_signal
 <222> 1072..1077

<220>
 <221> polyA_site
 <222> 1101..1115

<400> 93
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 ctcttttcaact gctagtaaga tcagattgcg tttcttttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaaa aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaaaca aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
 gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
 Met His Phe Gly Leu Leu
 -15
 tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
 Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
 -10 -5 1
 gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
 Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
 5 10 15 20
 aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
 Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
 25 30 35
 aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
 Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
 40 45 50
 gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
 Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
 55 60 65
 agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
 Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
 70 75 80
 att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
 Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
 85 90 95 100
 gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
 Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
 105 110 115
 aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
 Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
 120 125 130
 gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783
 Ala Ile
 ccgaatggtt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
 actccgcaat caaccaagg tcccagcctt tttgttacaa aagaaggaac aaatgatggt 903
 tggaagaatg cggctcatat ttaccaagtc tttctgaacg ctttctgcat tcatgcatcc 963
 atgttctttc taggattgga tagcatttca tgccatgtt aatatattgtg cttttggcat 1023
 ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
 atattttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
 <211> 152

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..19

<400> 94
 Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 30 35 40 45
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys
 80 85 90
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
 95 100 105
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser
 110 115 120 125
 Ser Met Val Asp Ala Trp Ala Ile
 130

<210> 95
 <211> 1307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..252

<220>
 <221> CDS
 <222> 253..744

<220>
 <221> 3'UTR
 <222> 745..1307

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1292..1307

<400> 95
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 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
 gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
 -25 -20 -15
 tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339

Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
85 90 95 100
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
105 110 115
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
120 125 130
Asn Gln Gln Phe
135

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

<220>
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<222> 1..117

<220>
<221> CDS
<222> 118..504

<220>
<221> 3'UTR
<222> 505..1855

<220>
<221> polyA_signal
<222> 1819..1824

<220>
<221> polyA_site
<222> 1840..1855

<400> 97
tccccgggccg ccgccgttgc gctcgccgcg ctcgcactga agccccgggcc ctcgcgcgcc 60
gcggttcgcc ccgcagcctc gccccctgcc caccgaggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100 105
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
Ala

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cctcccaggc ccctgggggca gccctcccg cgcaggtttc aggtcccagg ccccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcaactgcg ccggcgccag ccacgcgctc acgcaggcct gttctatggg 734
cgagctgctg cagtgcgggt gccaggcgcc ccgcggggcg gcccctcccc ggccctccgg 794
cctgccccgg acccccggac ccctggccc cgcgggctcc ccggaaggca gcgccgcctg 854
ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914
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cgaggcgggc aggttgccg tgcggagcca cagcgcgacc gagtgcaaat gccacgggct 1034
gtcgggatca tgcgcgctgc gcacctgtg gcagaagctg cctccatttc gcgaggtggg 1094
cgcgcggctg ctggagcgct tccacggcg ctcacgcgct atgggcacca acgacggcaa 1154
ggccctgctg ccgcgcgtcc gcacgtcaa gccgccggcg cgagcggacc tcctctacgc 1214
cgccgattcg ccgcacttct gcgccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccgacact cagcggctgc gacctgctgt gctgcggccg 1334
cgggcaccgc caggagagcg tgcagctcga agagaactgc ctgtgccgct tccactggtg 1394
ctgctagtag cagtgccacc gctgccgtgt gcgcaaggag ctcagcctct gctgtgacc 1454
cgccgccggg ccgctagact gacttcgcgc agcgggtggt cgcacctgtg ggacctcagg 1514
gcaccggcac cgggcgcctc tcgcgcgtcg agcccagcct ctccctgcc aagcccaact 1574
cccagggtc tggaaatggg gagcgaggg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agtttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatgggtg gtgaggttag 1814
tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

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<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25 30 35 40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
75 80 85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90 95 100
Ala
105

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<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

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<220>
<221> CDS

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<222> 95..613

<220>

<221> 3'UTR

<222> 614..667

<220>

<221> polyA_signal

<222> 636..641

<220>

<221> polyA_site

<222> 652..667

<400> 99

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gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
                               Met Ile Val Lys Gly Val Ala
                               1       5
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
      10       15       20
tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
      25       30       35
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
      40       45       50       55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
      60       65       70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
      75       80       85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
      90       95      100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
     105     110     115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
     120     125     130     135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
     140     145     150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
     155     160     165
caa acc act gtg aaa aat tagcttttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn
     170
tcttttcgcaa aaaaaaaaaa aaaa 667
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<210> 100

<211> 173

<212> PRT

<213> Homo sapiens

<400> 100

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Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
1       5       10      15
Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
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ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
      75      80      85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
      90      95      100
cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510
Arg Leu Phe Ser Asp Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp
     105     110     115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc 558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
    120     125     130     135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag 606
Lys Lys Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
      140      145      150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg 659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
      155      160
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatac gcccagatgg 719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg 779
acgttccacc attgtgattt gttcctgccc caccttaact gactgattaa cctgtgaat 839
ttccttctcc tggtcagaa gtcctccacc tgagcacctt gtgacccct gcccctgccc 899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaata ctataaaacg 959
gccccacccc tatctccctt tgctgactct cttttcggac tcagcccacc tgcagccagg 1019
tgaaaaaaac agctttattg ctcacacaaa aaaaaaaaaa aaa 1062

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<210> 102
 <211> 162
 <212> PRT
 <213> Homo sapiens

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<400> 102
Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Leu Trp Lys Asn Leu Thr
1      5      10      15
Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
20     25     30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
35     40     45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
50     55     60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
65     70     75     80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
85     90     95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
100    105    110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
115    120    125
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
130    135    140
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
145    150    155    160
Leu Leu

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<210> 103
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..149

<220>
 <221> CDS
 <222> 150..392

<220>
 <221> 3'UTR
 <222> 393..933

<220>
 <221> polyA_site
 <222> 63..933

<400> 103
 aaaccctcag ggacctggta tagacgcaga atctgtttca cacaacaact gctatttgaa 60
 ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
 cagatgtgta cggatgaaaa tacagtggag atg agt cag aaa ccg gcc aag gag 173
 Met Ser Gln Lys Pro Ala Lys Glu
 1 5
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
 10 15 20
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
 25 30 35 40
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
 45 50 55
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
 60 65 70
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
 Lys Ile Arg Pro Thr Pro Lys Lys Lys
 75 80
 ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472
 agttatatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
 gctcatgggtc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
 tcatcccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
 atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
 tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
 gcgtgggtggc gggcgctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
 gaacctggga ggcggagctt gcagtgagcc gagatcgac cactgcactc cagcctgggc 892
 gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933

<210> 104
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
 1 5 10 15
 Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
 20 25 30
 Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
 35 40 45
 Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
 50 55 60
 Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
 65 70 75 80
 Lys

<210> 105
 <211> 1187

<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..34

<220>
<221> CDS
<222> 35..1069

<220>
<221> 3'UTR
<222> 1070..1187

<220>
<221> polyA_signal
<222> 1146..1151

<220>
<221> polyA_site
<222> 1172..1187

<400> 105
accactttgg tagtgccagt gtgactcatc caca atg att tct cca gtg ctc atc 55
Met Ile Ser Pro Val Leu Ile
-15
ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
-10 -5 1 5
ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
10 15 20
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
25 30 35
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
40 45 50
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala
55 60 65
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro
70 75 80 85
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
90 95 100
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro
105 110 115
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala
120 125 130
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg
135 140 145
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn
150 155 160 165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu
170 175 180

tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt 679
 Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe
 185 190 195
 gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca 727
 Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr
 200 205 210
 ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa 775
 Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu
 215 220 225
 tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct 823
 Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser
 230 235 240 245
 tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga 871
 Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg
 250 255 260
 gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa 919
 Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys
 265 270 275
 gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag 967
 Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu
 280 285 290
 gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag 1015
 Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys
 295 300 305
 gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag 1063
 Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys
 310 315 320 325
 cca tgc taagggtgggtt ttcagattcc acataaaaatg tcacacttgt ttcttgttca 1119
 Pro Cys
 tccaaggaac ctaattgaaa tttaaaaaata aagctactga atttattgcc gcaaaaaaaa 1179
 aaaaaaaa 1187

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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..19

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 Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr
 15 20 25
 Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe
 30 35 40 45
 Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr
 50 55 60
 Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg
 65 70 75
 Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr
 80 85 90
 Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly
 95 100 105
 Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro
 110 115 120 125
 Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala
 130 135 140
 Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro

Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln
 400 405 410
 gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc 1299
 Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu
 415 420 425
 agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc 1347
 Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser
 430 435 440
 ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa 1395
 Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys
 445 450 455 460
 cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc 1443
 Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile
 465 470 475
 cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaaa aatctcttct 1499
 Gln Leu
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 <211> 478
 <212> PRT
 <213> Homo sapiens

<400> 108
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 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
 35 40 45
 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
 50 55 60
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
 65 70 75 80
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
 85 90 95
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
 100 105 110
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
 115 120 125
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
 130 135 140
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu
 145 150 155 160
 Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser
 165 170 175
 Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe
 180 185 190
 Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly
 195 200 205
 Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg
 210 215 220
 Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val
 225 230 235 240
 Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr
 245 250 255
 Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala
 260 265 270
 Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala
 275 280 285
 Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu
 290 295 300
 Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly

			45				50				55						
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Tyr	Gln	Ser	Asp	Glu	Thr	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Met	Leu	Leu		
			60				65				70						
aac	ggg	att	gtg	gac	cct	gct	gtc	atg	gga	ggc	ttc	gcc	aag	tat	gag		403
Asn	Gly	Ile	Val	Asp	Pro	Ala	Val	Met	Gly	Gly	Phe	Ala	Lys	Tyr	Glu		
			75				80				85						
aag	gcc	ttc	ttc	act	gaa	gag	tat	gtc	agg	gac	cac	cct	gag	gac	cag		451
Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val	Arg	Asp	His	Pro	Glu	Asp	Gln		
					95				100						105		
gac	aag	ctg	acc	cac	ctc	aag	gac	ctg	att	gca	tgg	cag	atc	ccc	ttc		499
Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu	Ile	Ala	Trp	Gln	Ile	Pro	Phe		
				110					115						120		
ttg	gga	gct	ggg	att	aag	atc	cat	gag	aaa	agg	gtg	tca	gat	aac	ttg		547
Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu	Lys	Arg	Val	Ser	Asp	Asn	Leu		
			125					130							135		
cga	ccc	ttc	cat	gac	cgg	atg	gag	gaa	tgt	ttc	aag	aac	ctg	aaa	atg		595
Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Glu	Cys	Phe	Lys	Asn	Leu	Lys	Met		
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Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg	Glu	Met	Pro	Asp	Phe	Asp	Asp		
			155				160				165						
agg	aga	gtg	ggc	cgt	ccc	agg	tct	atg	ctg	cgc	tca	tac	aga	cag	atg		691
Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met	Leu	Arg	Ser	Tyr	Arg	Gln	Met		
					175				180						185		
tcc	atc	atc	tct	ctg	gct	tcc	atg	aat	tct	gac	tgc	agc	acc	ccc	agc		739
Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn	Ser	Asp	Cys	Ser	Thr	Pro	Ser		
				190					195						200		
aag	cct	acc	tca	gag	agc	ttt	gac	ctg	gaa	tta	gca	tca	ccc	aag	acg		787
Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu	Glu	Leu	Ala	Ser	Pro	Lys	Thr		
			205					210							215		
ccg	aga	gtg	gag	cag	gag	gaa	ccg	atc	tcc	ccg	ggg	agc	acc	ctg	cct		835
Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile	Ser	Pro	Gly	Ser	Thr	Leu	Pro		
			220				225				230						
gag	gtc	aag	ctg	cgg	agg	tcc	aag	aag	agg	aca	aag	aga	agc	agc	gta		883
Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys	Arg	Thr	Lys	Arg	Ser	Ser	Val		
						240					245						
gtt	ttt	gcg	gat	gag	aaa	gca	gct	gca	gag	tcg	gac	ctg	aag	cgg	ctt		931
Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala	Glu	Ser	Asp	Leu	Lys	Arg	Leu		
					255				260						265		
tcc	agg	aag	cat	gag	ttc	atg	agt	gac	acc	aac	ctc	tcg	gag	cat	gcg		979
Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp	Thr	Asn	Leu	Ser	Glu	His	Ala		
				270					275						280		
gcc	atc	ccc	ctc	aag	gcg	tct	gtc	ctc	tct	caa	atg	agc	ttt	gcc	agc		1027
Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu	Ser	Gln	Met	Ser	Phe	Ala	Ser		
				285				290							295		
cag	tcc	atg	cct	acc	atc	cca	gcc	ctg	gcg	ctc	tca	gtg	gca	ggc	atc		1075
Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu	Ala	Leu	Ser	Val	Ala	Gly	Ile		
			300				305								310		
cct	ggg	ttg	gat	gag	gcc	aac	aca	tct	ccc	cgc	ctc	agc	cag	acc	ttc		1123
Pro	Gly	Leu	Asp	Glu	Ala	Asn	Thr	Ser	Pro	Arg	Leu	Ser	Gln	Thr	Phe		
			315				320				325						
ctc	caa	ctc	tca	gat	ggt	gac	aag	aag	aca	ctc	aca	cgg	aag	aag	gtc		1171
Leu	Gln	Leu	Ser	Asp	Gly	Asp	Lys	Lys	Thr	Leu	Thr	Arg	Lys	Lys	Val		
					335				340						345		
aat	cag	ttc	ttc	aag	aca	atg	ctg	gcc	agc	aaa	tcg	gct	gaa	gaa	ggc		1219
Asn	Gln	Phe	Phe	Lys	Thr	Met	Leu	Ala	Ser	Lys	Ser	Ala	Glu	Glu	Gly		
				350				355							360		
aaa	cag	atc	cca	gac	tcg	ctg	tcc	acg	gac	ctg	tgagctgctg	ctgactaggg					1272
Lys	Gln	Ile	Pro	Asp	Ser	Leu	Ser	Thr	Asp	Leu							
			365				370										
ctgcatggga	gagccaggga	ggggagtttc	tggaagagga	aagccatgcg	tggaacatcg												1332
aagcctcaga	gagtgaggaga	ctgtcccat	cagttgtcct	tacttagagg	agacagagag												1392

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gccaatcagg tcccagagct tgaatgctaa caagcccagc atccccctggg gctgtgatca 1452
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ctcccagtggt gctctcccca acatcctagg cacagctttc ataaccagc ttcttaggtg 1572
taagaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632
taaatattct ttttaatttt atttttagatt aacagttttg tactttacat ttttttatac 1692
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<210> 110

<211> 386

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..15

<400> 110

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Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
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Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
35 40 45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50 55 60 65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
70 75 80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
85 90 95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
100 105 110
Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
115 120 125
Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
130 135 140 145
Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
150 155 160
Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
165 170 175
Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
180 185 190
Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
195 200 205
Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
210 215 220 225
Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
230 235 240
Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
245 250 255
Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
260 265 270
Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
275 280 285
Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
290 295 300 305
Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
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Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
325 330 335
Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala

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Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val	
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atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt	642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu	
165 170 175 180	
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act	690
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr	
185 190 195	
gtg gag gtc aca aag acg ttt ttg cct ctt aga aaa tcc aaa ggg	738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly	
200 205 210	
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg	786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg	
215 220 225	
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca	834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser	
230 235 240	
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc	882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile	
245 250 255 260	
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg	930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp	
265 270 275	
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag	978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln	
280 285 290	
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta	1026
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu	
295 300 305	
ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac	1074
Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp	
310 315 320	
atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca	1122
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro	
325 330 335 340	
ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att	1170
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile	
345 350 355	
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc	1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro	
360 365 370	
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc	1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro	
375 380 385	
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<210> 112

<211> 387

<212> PRT

<213> Homo sapiens

<400> 112

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Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys	
35 40 45	
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser	
50 55 60	

Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val	65	70	75	80
Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His	85	90	95	
Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly	100	105	110	
Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys	115	120	125	
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln	130	135	140	
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly	145	150	155	160
Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp	165	170	175	
Gly	Glu	Leu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn	180	185	190	
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg	195	200	205	
Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala	210	215	220	
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr	225	230	235	240
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys	245	250	255	
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr	260	265	270	
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro	275	280	285	
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	290	295	300	
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	305	310	315	320
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	325	330	335	
Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	340	345	350	
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	355	360	365	
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	370	375	380	
Lys	Ala	Pro														385			